

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: September 17, 2003, 16:23:50 ; Search time 396.32 seconds

(without alignments)  
16618.183 Million cell updates/sec

Title: US-10-026-106e-7

Perfect score: 1599

Sequence: 1 aaggccatgagcgggcccga.....acatccaccgaatcgtatg 1599

Scoring table:

IDENTITY\_NUC  
Gapop 10.0, Gapext 1.0

Searched:

2888711 seqs, 2045481386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database:

GenEmbl:  
1: gb\_da:  
2: gb\_hg:  
3: gb\_in:  
4: gb\_om:  
5: gb\_ov:  
6: gb\_pac:  
7: gb\_ph:  
8: gb\_pl:  
9: gb\_pr:  
10: gb\_ro:  
11: gb\_scs:  
12: gb\_sy:  
13: gb\_un:  
14: gb\_vl:  
15: em\_ba:  
16: em\_fun:  
17: em\_hum:  
18: em\_in:  
19: em\_mu:  
20: em\_om:  
21: em\_or:  
22: em\_ov:  
23: em\_pac:  
24: em\_ph:  
25: em\_pl:  
26: em\_ro:  
27: em\_scs:  
28: em\_un:  
29: em\_vl:  
30: em\_hg\_hum:  
31: em\_hg\_inv:  
32: em\_hg\_other:  
33: em\_hg\_mus:  
34: em\_hg\_pln:  
35: em\_hg\_rtd:  
36: em\_hg\_mam:  
37: em\_hg\_vtc:  
38: em\_sy:  
39: em\_hgo\_hum:  
40: em\_hgo\_mus:  
41: em\_hgo\_other:

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1586.4	99.2	1607	9	HSAS34330
2	1580.4	98.8	4536	9	AF439325
3	1549.4	96.9	1563	6	AX478514
4	1549.4	96.9	1563	9	AY129151
5	1365.4	85.4	1476	9	AY129152
6	1354.2	84.7	1476	6	AX478492
7	1316	82.3	1476	9	HSAS34331
8	1086.8	68.0	1560	6	AX478524
9	916.2	57.3	1473	6	AX478499
10	784.4	49.7	164684	9	AL590683
11	783.8	49.0	1608	10	AY184376
12	609.4	38.1	1922	6	AX478528
13	607.4	38.0	1422	6	AX478518
14	498	31.1	674	6	AX478516
15	498	31.1	674	9	AY129153
16	498	31.1	704	6	AX497167
17	351.2	22.0	633	6	AX478525
18	335.4	21.0	374	6	AX069744
19	326.6	20.4	165515	10	AL662911
20	297	18.6	21062	2	AC133354
21	297	18.6	268510	2	AC095840
22	165	10.3	392	6	AX070906
23	163.4	10.2	382	6	AX070806
24	69.4	4.3	321	10	RNO230890
25	65	4.1	125020	9	AF429315
26	57.8	3.6	125020	9	AF429315
27	49.4	3.1	154855	2	AC119782
28	49.2	3.1	213335	2	AC11961
29	48.8	3.1	242385	2	AC103435
30	47.4	3.0	2000	6	AX655393
31	47.4	3.0	250498	2	AC111813
32	47.2	3.0	110000	2	AC144941-1
33	47.2	3.0	176789	2	AC032013
34	47.2	3.0	217092	10	AL590868
35	47	2.9	227202	2	AC128501
36	46.8	2.9	227182	2	AC099283
37	46.6	2.9	242648	2	AC128576
38	46.2	2.9	256511	2	AC123662
39	46	2.9	242857	2	AC096180
40	45.8	2.9	260809	2	AC126820
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ALIGNMENTS

RESULT 1  
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DEFINITION Homo sapiens mRNA for likely Interleukin or Cytokine Receptor 2  
ACCESSION AJ534330  
VERSION AJ534330.1 GI:26986037  
KEYWORDS L1CR2 gene; Likely Interleukin or Cytokine Receptor 2.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
REFERENCE 1  
Dumoutier, L., Lejume, D., Hor, S., Rickenscher, H. and Renauld, J.C.  
TITLE Cloning of a new type II cytokine receptor activating signal





Dp	121	TTGACATGCGTCCCAAGGGCTTGGCAACCCCCAGATGAGACCTAATTTTGTGGCTATCAG	180
Qy	186	AGCTCTCCCAACCCGTTAAGACGGTGGCGGCAAGTGAAGAGTGTGGGGAAACAAAGSAGTG	245
Dp	181	AGCTCTCCCAACCCGTTAAGACGGTGGCGGCAAGTGAAGAGTGTGGGGAAACAAAGSAGTG	240
Qy	246	CTATGTTCTATGATGATGTGCTGAGAGAAACAGACCTGTACAAACAAGTTCAAGGACGCGTG	305
Dp	241	CTAATGTTCTATGATGATGTGCTGAGAGAAACAGACCTGTACAAACAAGTTCAAGGAGCGCTG	300
Qy	306	CGACGGGTTTCTCCAGAGCTCCAGAGTCCCCCTGGGTGAGTCCGAAATACCTGSAATTACCTT	365
Dp	301	CGACGGGTTTCTCCAGAGCTCCAGAGTCCCCCTGGGTGAGTCCGAAATACCTGSAATTACCTT	360
Qy	366	TTTGAAGTGAAGACGGGGCCCACTGTGCTGTGGTGTCAACCGAAGAGAGAGATCCGAGT	425
Dp	361	TTTGAAGTGAAGACGGGGCCCACTGTGCTGTGGTGTCAACCGAAGAGAGATCCGAGT	420
Qy	426	GCCAATGCCAGTACACAGCTGTCGCCCTCTGATGCCCCCACTGATTTGAAGTGAAGTG	485
Dp	421	GCCAATGCCAGTACACAGCTGTCGCCCTCTGATGCCCCCACTGATTTGAAGTGAAGTG	480
Qy	486	GCATTTCTGAGAGAGAGGGGGCGGAAACAAGACCTTAATTTCCAGTCACTCCCCATGGCCAG	545
Dp	481	GCATTTCTGAGAGAGAGGGGGCGGAAACAAGACCTTAATTTCCAGTCACTCCCCATGGCCAG	540
Qy	546	CCAGTCCAGATCATCTCTCAAGCCAGAGCTGCCACCGAACAACATCTGCTCAAGTGCAGAAAC	605
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Qy	606	ATCTACACGTTGACGTGTCCCGAAATAACAGCAAGTTCTGTAAAGCCCACTGCTCTTGTGTG	665
Dp	601	ATCTACACGTTGACGTGTCCCGAAATAACAGCAAGTTCTGTAAAGCCCACTGCTCTTGTGTG	660
Qy	666	GAGGTCCCGAAGAGCGAATGGGGCTTTCTGTGGTGTGAGCATGCTCTGTGAATCTGCTGTTA	725
Dp	661	GAGGTCCCGAAGAGCGAATGGGGCTTTCTGTGGTGTGAGCATGCTCTGTGAATCTGCTGTTA	720
Qy	726	GTAATTCGCGCAGGGGGGTGTATTTGGAAGACCTCTCATGGGAAACCTCTGGTTTCAAGCG	785
Dp	721	GTAATTCGCGCAGGGGGGTGTATTTGGAAGACCTCTCATGGGAAACCTCTGGTTTCAAGCG	780
Qy	786	GCAAGATGSCAACGGGACCTGGAATTTTCTGAGACACACACACCTGTGGCAACTTTTACG	845
Dp	781	GCAAGATGSCAACGGGACCTGGAATTTTCTGAGACACACACACCTGTGGCAACTTTTACG	840
Qy	846	CCGACGACACAGAGATCCGGAATGACTTGTTCCTGTGTCCCAAAAGAACTGACACGA	905
Dp	841	CCGACGACACAGAGATCCGGAATGACTTGTTCCTGTGTCCCAAAAGAACTGACACGA	900
Qy	906	GGGGTCAAGCCCAACGCTCTGAGTCAAGGGGCCCAAGCCACCTCAACAGACAGATGGAAGAG	965
Dp	901	GGGGTCAAGCCCAACGCTCTGAGTCAAGGGGCCCAAGCCACCTCAACAGACAGATGGAAGAG	960
Qy	966	GACCTTGCAGAGGAGAGAGAGAGATGAGAGAGACACAGAGATGAGCTCAGCTTC	1025
Dp	961	GACCTTGCAGAGGAGAGAGAGAGATGAGAGAGACACAGAGATGAGCTCAGCTTC	1020
Qy	1026	CAGCCCTCACTTGAACCAACTTTCTTTCTGTGGGCAAGACACAGAGTCCAGGGGCACTCG	1085
Dp	1021	CAGCCCTCACTTGAACCAACTTTCTTTCTGTGGGCAAGACACAGAGTCCAGGGGCACTCG	1080
Qy	1086	GAGGCTGTGGGTGAGACTCAAGGAGGCCCAAGGGCTCTCTGTGTCCAAAGCAAGGCTTC	1145
Dp	1081	GAGGCTGTGGGTGAGACTCAAGGAGGCCCAAGGGCTCTCTGTGTCCAAAGCAAGGCTTC	1140
Qy	1146	TCTCTTGGGATTTCTTCAAGACAGAAAGTGGGCAAGCATGTGSACTCTCTTGGGACAG	1205
Dp	1141	TCTCTTGGGATTTCTTCAAGACAGAAAGTGGGCAAGCATGTGSACTCTCTTGGGACAG	1200
Qy	1206	GCTGGGATCTCTGTGCTAATTTGGCTTGAGAAAGGGCCAAAGGCCGGGTGGGATGGG	1265
Dp	1201	GCTGGGATCTCTGTGCTAATTTGGCTTGAGAAAGGGCCAAAGGCCGGGTGGGATGGG	1260









Qy	666	GAGGTCCGAAAGCCAACTGGGCTTTCTGAGGCTGGCAATGCGTTGATATGCTGTGA	725
Db	661	GAGGTCCGAAAGCCAACTGGGCTTTCTGAGGCTGGCAATGCGTTGATATGCTGTGA	720
Qy	726	GTAATTGCGCCAGGGGGGTGTGATCTGGAAGACCCCTCATGGGGAACCCCTGTTCAGCG	785
Db	721	GTAATTGCGCCAGGGGGGTGTGATCTGGAAGACCCCTCATGGGGAACCCCTGTTCAGCG	780
Qy	786	GCAAGAATGCGACGGGGCCCTGGAATTTCGTGACACACACCTGTGGCAACTTTCAG	845
Db	781	GCAAGAATGCGACGGGGCCCTGGAATTTCGTGACACACACCTGTGGCAACTTTCAG	840
Qy	846	CCGACGACAGACAGAGTCCGTGATGACTGTGTCTGTGCTCCCAAAAGAACTGACAGA	905
Db	801	-----GAACTGACAGA 813	
Qy	906	GGGGTCAGGCGCCAGCGCTTGAGTCAAGGGCCCCAGCCACCCAAACAGACAGATGGAAAG	965
Db	814	GGGGTCAGGCGCCAGCGCTTGAGTCAAGGGCCCCAGCCACCCAAACAGATGGAAAG	873
Qy	966	GACCTTCAGAGAGCAGAGAGAGAGAGATGAGAGAGACAGAAAGTGGCCCTCAGCTTC	1025
Db	874	GACCTTCAGAGAGCAGAGAGAGAGAGATGAGAGAGACAGAAAGTGGCCCTCAGCTTC	933
Qy	1026	CAGCCCTACATTGAAACAACCTTCTTCTCTGGGGCAGAGACACAGGCTCCAGGGGACTCG	1085
Db	934	CAGCCCTACATTGAAACAACCTTCTTCTCTGGGGCAGAGACACAGGCTCCAGGGGACTCG	993
Qy	1086	GAGGCTGTGGGTGGATCTCAGAGAGGCCCAAGGGGCTCCGTGTGCCAAGGAGCTCC	1145
Db	994	GAGGCTGTGGGTGGATCTCAGAGAGGCCCAAGGGGCTCCGTGTGCCAAGGAGCTCC	1053
Qy	1146	TCGTCTGGGATTCCTTCAGACAGAAAGCTGGGCCAGACCTGTGACTCTCTCTGGGACAG	1205
Db	1054	TCGTCTGGGATTCCTTCAGACAGAAAGCTGGGCCAGACCTGTGACTCTCTCTGGGACAG	1113
Qy	1206	GCTGGGCTCTCTGGCTATTGGCTGAGAGGGGCAAGGCGCAGAGGGCGGGTGGGGATGGG	1265
Db	1114	GCTGGGCTCTCTGGCTATTGGCTGAGAGGGGCAAGGCGCAGAGGGCGGGTGGGGATGGG	1173
Qy	1266	CACCAAGATCTCTCCACCAACCTGAAATTCCTCCAAAGATCGGGGTTCTGTGAAGAGCTC	1325
Db	1174	CACCAAGATCTCTCTCCACCAACCTGAAATTCCTCCAAAGATCGGGGTTCTGTGAAGAGCTC	1233
Qy	1326	CCAGAAAGATTAACCTCTCTCTCTGGGCAACTGGGGCACTTACCAACGAGAGCCGAATCTG	1385
Db	1234	CCAGAAAGATTAACCTCTCTCTCTGGGCAACTGGGGCACTTACCAACGAGAGCCGAATCTG	1293
Qy	1386	GTTCCTGGGGGACCCCAAGTTCTCTTGAACACTGACCTTGTGTGGTGAAGAACAGCCCT	1445
Db	1294	GTTCCTGGGGGACCCCAAGTTCTCTTGAACACTGACCTTGTGTGGTGAAGAACAGCCCT	1353
Qy	1446	GAGGAGGAAGAGAGGCGAGGAGATCAGAAATTGAGACAGCGATGCGGAGCTGAGGG	1505
Db	1354	GAGGAGGAAGAGAGGCGAGGAGATCAGAAATTGAGAGCAGGATGCGGAGCTGAGGG	1413
Qy	1506	GCTGAGAGCACCAGAGAGACCGAGAGCAGGGGCGGACATGTGGGCAATTACATGGCCAG	1565
Db	1414	GCTGAGAGCACCAGAGAGACCGAGAGCAGGGGCGGACATGTGGGCAATTACATGGCCAG	1473
Qy	1566	TGA 1568	
Db	1474	TGA 1476	

REFERENCE	AUTHORS	TITLE	JOURNAL	MEDLINE	REFERENCE	TITLE	FEATURES	source	gene	CDS
1	Dumontier, L., Lejeune, D., Hor, S., Plickenscher, H. and Renaud, J. C.	Cloning of a new type II cytokine receptor activating signal transducer and activator of transcription (STAT)1, STAT2 and STAT3	Biochem. J. 370 (Pt 2), 391-396 (2003)	22478845	2	(bases 1 to 1476)	Direct Substitution	Submitted (06-DEC-2002) Renaud J. C., UCL 74.59, Ludwig Institute for Cancer Research, 74 Avenue Hippocrate, B-1200 Brussels, BELGIUM		
2	Renaud, J. C.			12521379	2	(bases 1 to 1476)				
3					3					
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Qy	606	ATCTACAGCTTCACTGCTCCGAAATATACAGCAAGTCTCTAAGCCACCTGCTCTGCTG	665			
Db	601	ATHTATACNTTYTWSNGTNCNNAATATAYMSNAARTTYMSNAARCAACNTGYTYTYTN	660			
Qy	666	GAGGTCCAGAAAGGAACTGGGGCTTCTCTGCTGTCGCATCGCTTCTGATACTGCTT	725			
Db	661	GARGTNCNCGARGCMAAYTGGCCNTTYTYNGTNTYTNCCMSNTYNTAHTYNTYTN	720			
Qy	726	GPATATTCGACGGGGGTGTGATCTTGAAAGACCTCACTGGGGAACCCCTGGTTTCA	785			
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Qy	786	GCMAAGATGCCAGGGGCTTGACCTTTCTGCAACACACACCTCTGTGCAACTTT	845			
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Qy	846	CCACACAGACACAGAGTCCTGATGATGACTTGTCTCTGTCCTCCCAAAAGAACTG	905			
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Qy	906	GGGGTCAAGGGCCAGCCCTGATGATCAAGGGCCCCACCCACCAACAGCAAGATG	965			
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Qy	1026	CAGCCTTCAATTGACCACTTCTTCTCTGGGGGAAAGAGACAGAGCTTCAGGGCACTG	1081			
Db	1021	CARCCNTATYATHGARCCNCCMSNTTYTYTNGNCARBARATYACAGCMNCNCGNCA	1080			
Qy	1086	GAGCGTGTGGGTGTGATCTCAGGAGAGGCCAGGGCTCTCTGTGCCCAAGGAA	1141			
Db	1081	GATGNGNAGNGNGTNGATYMSNGNAGNCCNMGNCNCACTYTGTCNCCMSNGAR	1140			
Qy	1146	TTCTCTGGGATCTTCAAGCAAGCTGGGCCAGCATGTGTGACTCTCTCTGGGACAG	1201			
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Qy	1326	CCAGAAAGATACTCTCTCTCTCTGGGCCACTGGGGCACTTACCAACCGAGCC	1381			
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Qy	1386	GTCCCTGGGGGACCCCACTTCTCTTGAGACATGACCTTCGCTCGGGAAGAAG	1441			
Db	1381	GTNCNCGNNGNCCNCCNCTGMSNTYTNCAACNTTACNTTYTGTGGGA	1440			
Qy	1446	GAGAGAGAAAGAGAGCGGAGGAGATCAGAAATTGAGACGAGTGCAGGACGTGGGG	1501			
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Qy	1506	GCTGAGAGACCCAGAGAGACCGAGAGACGAGGGGCGGACATTTGAGGACATTA	1564			
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 1114 GCGGAGTGAAGTGAAGTGAAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1173  
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 1174 CAYCARGAGAGTGAAGTGAAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1233  
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 1446 GAGGAG 1505  
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 1506 GCTGAGAGACCCAG 1564  
 1414 GCGGAG 1472

RESULT 10  
 AL590683/c 164684 bp DNA linear PRI 01-FEB-2002  
 LOCUS Human DNA sequence from clone Rp11-10N16 on chromosome 1, complete  
 DEFINITION  
 accession AL590683  
 version AL590683.16 GI:18476679  
 keywords HTG.  
 SOURCE  
 ORGANISM Homo sapiens (human)  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 REFERENCE  
 AUTHORS Chapman, J.  
 TITLE Direct Submision  
 JOURNAL Submitted (01-FEB-2002) Wellcome Trust Sanger Institute, Hinxton,  
 Cambridgeshire, CB10 1SA, UK. E-mail enquiries:  
 humquer@sanger.ac.uk Clone requests: clonequest@sanger.ac.uk  
 On Feb 1, 2002 this sequence version replaced gi:18135066.

During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em, EMBL; Sw, SwissProt; Tr, TrEMBL; Wp, WormPeP; information on the WormPeP database can be found at [http://www.sanger.ac.uk/Projecte/C\\_elegans/wormpep](http://www.sanger.ac.uk/Projecte/C_elegans/wormpep) This sequence was generated from part of bacterial clone contigs of human chromosome 1, constructed by the Sanger Centre Chromosome 1 Mapping Group. Further information can be found at <http://www.sanger.ac.uk/HGP/Chr1> Rp11-10N16 is from the library RPICT-11.1 constructed by the group of Pictet de Jong. For further details see <http://www.chori.org/bacpac/home.htm> VECTOR: pBACE3.6

This sequence is the entire insert of clone Rp11-10N16 The true left end of clone Rp11-509P14 is at 17440 in this sequence. The true right end of clone Rp11-293P20 is at 7665 in this sequence.

FEATURES

source

1. 164684

/organism="Homo sapiens"

/mol\_type="Genomic DNA"

/db\_xref="taxon:9606"

/chromosome="1"

/clone="Rp11-10N16"

/clone\_1lb="RPICT-11.1"

51656..51817

/note="Sequence from overlapping clone Rp11-509P14 (AL358412). Assembly confirmed by restriction digest."

misc\_feature

76735..77049

/note="Single clone region. Reads generated from a transposon library derived from a single pUC clone. Restriction digest data confirm the assembly."

94068..94090

/note="Sequence from overlapping clone Rp11-509P14 (AL358412). Assembly confirmed by restriction digest."

misc\_feature

42390 a 38933 c 39092 g 44269 t

BASE COUNT

ORIGIN

Query Match 49.7% Score 794.4; DB 9; Length 164684;

Best Local Similarity 99.9% Pred. No. 1.4e-193;

Matches 795; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

804 CTGACCTTTCTGAGACACACCTGTGAGACCTTGTGAGACCGGAGAGACGAGTCC 863

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 DEFINITION Sequence 32 from Patent WO0244209.  
 ACCESSION AX478528  
 VERSION AX478528.1 GI:22217300  
 KEYWORDS  
 SOURCE synthetic construct  
 ORGANISM synthetic construct  
 ARTIFICIAL SEQUENCES.  
 REFERENCE  
 1 Presnell, S.R., Xu, W., Novak, J.E., Whitmore, T.E. and Grant, F.J.  
 Cytokine receptor zcytor19  
 Patent: WO 0244209-A-32 06-JUN-2002;  
 Zymogenetics, Inc. (US)

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 Best Local Similarity 97.4%; Pred. No. 7.7e-146;  
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DEFINITION Sequence 22 from Patent WO0244209.  
ACCESSION AX478518  
VERSION AX478518.1 GI:22217290  
KEYWORDS  
SOURCE  
ORGANISM  
synthetic construct  
artificial sequences.

REFERENCE  
1. Prensell, S.R., Xu, W., Novak, J.E., Whitmore, T.E. and Grant, F.J.  
AUTHORS  
TITLE Cytokine receptor zcytor19  
JOURNAL Patent: WO 0244209-A 22 06-JUN-2002;  
Zymogenetics, Inc. (US)  
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BASE COUNT 331 a 451 c 377 g 263 t  
ORIGIN

Query Match 38.0%; Score 607.4; DB 6; Length 1422;  
Best Local Similarity 99.7%; Pred. No. 2.5e-145;  
Matches 619; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

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Db 186 AAGCTCTCCACCGTAGACGGTGGCGGAGAGTGAAGTGTGGGAGAACAGAGAGCTG 245

Qy 229 AAGCTCTCCACCGTAGACGGTGGCGGAGAGTGAAGTGTGGGAGAACAGAGAGCTG 288

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ACCESSION AX478516  
VERSION AX478516.1 GI:22217288  
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SOURCE  
ORGANISM  
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

REFERENCE  
1. Prensell, S.R., Xu, W., Novak, J.E., Whitmore, T.E. and Grant, F.J.  
AUTHORS  
TITLE Cytokine receptor zcytor19  
JOURNAL Patent: WO 0244209-A 20 06-JUN-2002;  
Zymogenetics, Inc. (US)  
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Query Match 31.1%; Score 498; DB 6; Length 674;  
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ACCESSION	Ay129153			
VERSION	Ay129153.1			
KEYWORDS	GI:2552735			
SOURCE	Homo sapiens (human)			
ORGANISM	Homo sapiens			

SOURCE	ORGANISM
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.	1 (Homo sapiens)

REFERENCE  
AUTHORS  
1 (bases 1 to 674)  
Sheppard, P.O., Presnell, S.R., Fox, B.A., Gilbert, T., Haldeman, B.A.

TITLE	INVENTOR	ATTORNEY
IL28RA splice variant 3	and Grant, F.J.	Stadel, R., Hauelmann, D.A.

JOURNAL	ISSUE	PAGE	DATE
Unpublished			
2 (bases 1 to 674)			

2 (bases 1 to 6/4)  
Sheppard, P.O., Presnell, S.R., Fox, B.A., Gilbert, T., Haldeman, B.A., and Grant, F.J.

**TITLE** and Grant, F. J.  
**JOURNAL** Direct Submission  
Submitted (05-Jul-2003) Refereed (06-Aug-2003)  
Revised (07-Sep-2003) Accepted (08-Oct-2003)

**JOURNAL**  
Submitted (05-JUL-2002) Bioinformatics, ZymoGenetics, Inc., 1201  
Eastlake Avenue East, Seattle, WA 98102, USA  
Received (05-JUL-2002)

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